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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/765,588

DATE: 09/01/98
TIME: 16:14:03

Input Set: H765588.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

new format

1 <110> APPLICANT: Hayward, Nicholas K.
2 Weber, Gunther
3 Grimmond, Sean
4 Nordenskjold, Magnus
5 Larsson, Catharina
6 <120> TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
7 SAME
8 <130> FILE REFERENCE: DAVIES
9 <140> CURRENT APPLICATION NUMBER: US/08/765,588
10 <141> CURRENT FILING DATE: 1997-04-25
11 <160> NUMBER OF SEQ ID NOS: 23
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 649
15 <212> TYPE: DNA
16 <213> ORGANISM: Nucleotide Sequence of VEGF165
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23 1 5 10
24 gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100
25 Ala Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
26 15 20 25
27 atg gca gaa gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148
28 Met Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
29 30 35 40
30 gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196
31 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
32 45 50 55 60
33 atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244
34 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
35 65 70 75
36 tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg 292
37 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
38 80 85 90
39 gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340
40 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
41 95 100 105
42 atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag 388
43 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
44 110 115 120

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45 cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa 436
 46 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
 47 125 130 135 140
 48 sat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa 484
 49 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
 50 145 150 155
 51 gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc 532
 52 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
 53 160 165 170
 54 aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag 580
 55 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
 56 175 180 185
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 60 gaaccagatc tctcaccagg 649
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 67 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 68 20 25 30
 69 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 70 35 40 45
 71 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 72 50 55 60
 73 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 74 65 70 75 80
 75 Met Arg Cys Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 76 85 90 95
 77 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 78 100 105 110
 79 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 80 115 120 125
 81 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 82 130 135 140
 83 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 84 145 150 155 160
 85 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 86 165 170 175
 87 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 88 180 185 190
 89
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 91 <211> LENGTH: 1094
 92 <212> TYPE: DNA
 93 <213> ORGANISM: Nucleotide Sequence of SOM175
 94 <220> FEATURE:

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 100 1 5 10 15
 101 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 102 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 103 20 25 30
 104 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 105 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 106 35 40 45
 107 cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 108 Gln Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 109 50 55 60
 110 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 111 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 112 65 70 75
 113 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 114 Gly Cys Cys Pro Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 115 80 85 90 95
 116 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
 117 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 118 100 105 110
 119 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
 120 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 121 115 120 125
 122 aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac 431
 123 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
 124 130 135 140
 125 cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca 479
 126 Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
 127 145 150 155
 128 ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
 129 Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
 130 160 165 170 175
 131 gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc 575
 132 Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
 133 180 185 190
 134 gct gcc gct gcc gac gca gct tcc tcc gtt gcc aag ggc ggg gct 623
 135 Ala Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 136 195 200 205
 137 tagagctcaa cccagacacc tgcatgggcc ggaagctcg aaggtgacac atggctttc 683
 138 agactcagca gggtaacttg cctcagaggc tatatcccag tggggaaaca aaggggagcc 743
 139 tggtaaaaaa cagccaagcc cccaaacacct cagccccagcc agaagctgct ctaggacactg 803
 140 ggcctctcag agggctcttc tgccatccct tgcctccctg aggccatcat caaacagac 863
 141 agagttggaa gaggagactg ggagggcagca agaggggtca cataccagct caggggagaa 923
 142 tggagtactg tctcagtttc taaccactt gtcagaatgaa gcatcttaca actggctt 983
 143 cctccccccta ctaagaagac ccaaacctct gcataatggg atttggctt tggtaacaaga 1043
 144 actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

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145 <210> SEQ ID NO 4
 146 <211> LENGTH: 207
 147 <212> TYPE: PRT
 148 <213> ORGANISM: Nucleotide Sequence of SOM175
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 151 1 5 10 15
 152 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 153 20 25 30
 154 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 155 35 40 45
 156 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 157 50 55 60
 158 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 159 65 70 75 80
 160 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 161 85 90 95
 162 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 163 100 105 110
 164 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 165 115 120 125
 166 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 167 130 135 140
 168 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 169 145 150 155 160
 170 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
 171 165 170 175
 172 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
 173 180 185 190
 174 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 175 195 200 205

176 <210> SEQ ID NO 5
 177 <211> LENGTH: 993
 178 <212> TYPE: DNA
 179 <213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6
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 181 <221> NAME/KEY: CDS
 182 <222> LOCATION: (3)..(566)
 183 <400> SEQUENCE: 5
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 186 1 5 10 15
 187 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 188 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 189 20 25 30
 190 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 191 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 192 35 40 45
 193 cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 194 Gln Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr

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196	gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt			239
197	Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly			
198	65	70	75	
199	ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac			287
200	Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His			
201	80	85	90	95
202	caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg			335
203	Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu			
204	100	105	110	
205	ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa			383
206	Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys			
207	115	120	125	
208	aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca			431
209	Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro			
210	130	135	140	
211	cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc			479
212	Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys			
213	145	150	155	
214	cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag			527
215	Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu			
216	160	165	170	175
217	ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg			576
218	Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg			
219	180	185		
220	ctttcagac tcagcagggt gacttgccctc agaggctata tcccagtggg ggaacaaaagg	636		
221	ggagcctgggt aaaaaacagc caagccccca agacctcagc ccaggcagaa gctgctctag	696		
222	gacctgggcc tctcagaggg ctcttctgcc atcccattgtc tccctgaggg catcatcaaa	756		
223	caggacagag ttggaagagg agactggag gcagcaagag gggtcacata ccagctcagg	816		
224	ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg	876		
225	gctcttcctc ccctcaactaa gaagacccaa acctctgcat aatgggattt gggcttttgt	936		
226	acaagaactg tgaccccca ccctgataaa agagatggaa ggaaaaaaaaaaaaaaaaa	993		
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228	<211> LENGTH: 188			
229	<212> TYPE: PRT			
230	<213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6			
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234	Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln			
235	20	25	30	
236	Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln			
237	35	40	45	
238	Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val			
239	50	55	60	
240	Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly			
241	65	70	75	80
242	Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln			
243	85	90	95	
244	Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly			

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